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Microarray analysis identification of key pathways and interaction network of differential gene expressions during osteogenic differentiation

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Abstract

Background: Adult bone marrow-derived mesenchymal stem cells (BM-MSCs) are multipotent stem cells that can differentiate into three lineages. They are suitable sources for cell-based therapy and regenerative medicine applications. This study aims to evaluate the hub genes and key pathways of differentially expressed genes (DEGs) related to osteogenesis by bioinformatics analysis in three different days. The DEGs were derived from the three different days compared with day 0.

Results: Gene expression profiles of GSE37558 were obtained from the Gene Expression Omnibus (GEO) database. A total of 4076 DEGs were acquired on days 8, 12, and 25. Gene ontology (GO) enrichment analysis showed that the non-canonical Wnt signaling pathway and lipopolysaccharide (LPS)-mediated signaling pathway were commonly upregulated DEGs for all 3 days. KEGG pathway analysis indicated that the PI3K-Akt and focal adhesion were also commonly upregulated DEGs for all 3 days. Ten hub genes were identified by CytoHubba on days 8, 12, and 25. Then, we focused on the association of these hub genes with the Wnt pathways that had been enriched from the protein-protein interaction (PPI) by the Cytoscape plugin MCODE.

Conclusions: These findings suggested further insights into the roles of the PI3K/AKT and Wnt pathways and their association with osteogenesis. In addition, the stem cell microenvironment via growth factors, extracellular matrix (ECM), IGF1, IGF2, LPS, and Wnt most likely affect osteogenesis by PI3K/AKT.

Keywords: Bone mesenchymal stem cells, Bioinformatics analysis, Osteogenic differentiation, Protein-protein network

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